

0219us410-sequence.txt
SEQUENCE LISTING

<110> Maxygen Aps; Maxygen Holding

<120> Protein C or activated protein C-like molecules

<130> 0219us410 - protein C

<140>

<141>

<160> 40

<170> PatentIn Ver. 2.1

<210> 1

<211> 1383

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1383)

<220>

<221> mat_peptide

<222> (127)..(1383)

<400> 1

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Met	Trp	Gln	Leu	Thr	Ser	Leu	Leu	Leu	Phe	Val	Ala	Thr	Trp	Gly	Ile	
		-40					-35					-30				

tcc	ggc	aca	cca	gct	cct	ctt	gac	tca	gtg	ttc	tcc	agc	agc	gag	cgt	96
Ser	Gly	Thr	Pro	Ala	Pro	Leu	Asp	Ser	Val	Phe	Ser	Ser	Ser	Glu	Arg	
	-25					-20					-15					

gcc	cac	cag	gtg	ctg	cgg	atc	cgc	aaa	cgt	gcc	aac	tcc	ttc	ctg	gag	144
Ala	His	Gln	Val	Leu	Arg	Ile	Arg	Lys	Arg	Ala	Asn	Ser	Phe	Leu	Glu	
-10					-5				-1	1				5		

gag	ctc	cgt	cac	agc	agc	ctg	gag	cgg	gag	tgc	ata	gag	gag	atc	tgt	192
Glu	Leu	Arg	His	Ser	Ser	Leu	Glu	Arg	Glu	Cys	Ile	Glu	Glu	Ile	Cys	
			10					15					20			

gac	ttc	gag	gag	gcc	aag	gaa	att	ttc	caa	aat	gtg	gat	gac	aca	ctg	240
Asp	Phe	Glu	Glu	Ala	Lys	Glu	Ile	Phe	Gln	Asn	Val	Asp	Asp	Thr	Leu	
		25					30					35				

gcc	ttc	tgg	tcc	aag	cac	gtc	gac	ggt	gac	cag	tgc	ttg	gtc	ttg	ccc	288
Ala	Phe	Trp	Ser	Lys	His	Val	Asp	Gly	Asp	Gln	Cys	Leu	Val	Leu	Pro	
	40					45					50					

ttg	gag	cac	ccg	tgc	gcc	agc	ctg	tgc	tgc	ggg	cac	ggc	acg	tgc	atc	336
Leu	Glu	His	Pro	Cys	Ala	Ser	Leu	Cys	Cys	Gly	His	Gly	Thr	Cys	Ile	
55					60					65					70	

gac	ggc	atc	ggc	agc	ttc	agc	tgc	gac	tgc	cgc	agc	ggc	tgg	gag	ggc	384
Asp	Gly	Ile	Gly	Ser	Phe	Ser	Cys	Asp	Cys	Arg	Ser	Gly	Trp	Glu	Gly	
				75				80						85		

cgc	ttc	tgc	cag	cgc	gag	gtg	agc	ttc	ctc	aat	tgc	tcg	ctg	gac	aac	432
Arg	Phe	Cys	Gln	Arg	Glu	Val	Ser	Phe	Leu	Asn	Cys	Ser	Leu	Asp	Asn	
			90				95						100			

ggc	ggc	tgc	acg	cat	tac	tgc	cta	gag	gag	gtg	ggc	tgg	cgg	cgc	tgt	480
Gly	Gly	Cys	Thr	His	Tyr	Cys	Leu	Glu	Glu	Val	Gly	Trp	Arg	Arg	Cys	

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105	110	115	
agc tgt gcg cct ggc tac aag ctg ggg gac gac ctc ctg cag tgt cac Ser Cys Ala Pro Gly Tyr Lys 125 Leu Gly Asp Asp Leu 130 Leu Gln Cys His			528
ccc gca gtg aag ttc cct tgt ggg agg ccc tgg aag cgg atg gag aag Pro Ala Val Lys Phe Pro 140 Cys Gly Arg Pro Trp 145 Lys Arg Met Glu Lys 150			576
aag cgc agt cac ctg aaa cga gac aca gaa gac caa gaa gac caa gta Lys Arg Ser His Leu 155 Lys Arg Asp Thr Glu 160 Asp Gln Glu Asp Gln Val 165			624
gat ccg cgg ctc att gat ggg aag atg acc agg cgg gga gac agc ccc Asp Pro Arg Leu 170 Ile Asp Gly Lys Met 175 Thr Arg Arg Gly Asp Ser Pro 180			672
tgg cag gtg gtc ctg ctg gac tca aag aag aag ctg gcc tgc ggg gca Trp Gln Val Val Leu Leu Asp Ser 190 Lys Lys Lys Leu Ala 195 Cys Gly Ala			720
gtg ctc atc cac ccc tcc tgg gtg ctg aca gcg gcc cac tgc atg gat Val Leu Ile His Pro Ser Trp 205 Val Leu Thr Ala 210 His Cys Met Asp			768
gag tcc aag aag ctc ctt gtc agg ctt gga gag tat gac ctg cgg cgc Glu Ser Lys Lys Leu Leu 220 Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg 230			816
tgg gag aag tgg gag ctg gac ctg gac atc aag gag gtc ttc gtc cac Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile 240 Lys Glu Val Phe Val His 245			864
ccc aac tac agc aag agc acc acc gac aat gac atc gca ctg ctg cac Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His 250 255 260			912
ctg gcc cag ccc gcc acc ctc tcg cag acc ata gtg ccc atc tgc ctc Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu 265 270 275			960
ccg gac agc ggc ctt gca gag cgc gag ctc aat cag gcc ggc cag gag Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu 280 285 290			1008
acc ctc gtg acg ggc tgg ggc tac cac agc agc cga gag aag gag gcc Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala 295 300 305 310			1056
aag aga aac cgc acc ttc gtc ctc aac ttc atc aag att ccc gtg gtc Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val 315 320 325			1104
ccg cac aat gag tgc agc gag gtc atg agc aac atg gtg tct gag aac Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn 330 335 340			1152
atg ctg tgt gcg ggc atc ctc ggg gac cgg cag gat gcc tgc gag ggc Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly 345 350 355			1200
gac agt ggg ggg ccc atg gtc gcc tcc ttc cac ggc acc tgg ttc ctg Asp Ser Gly Gly Pro Met Val 365 Ala Ser Phe His Gly Thr Trp Phe Leu 370			1248
gtg ggc ctg gtg agc tgg ggt gag ggc tgt ggg ctc ctt cac aac tac			1296

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Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
375 380 385 390

ggc gtt tac acc aaa gtc agc cgc tac ctc gac tgg atc cat ggg cac 1344
Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
395 400 405

atc aga gac aag gaa gcc ccc cag aag agc tgg gca cct 1383
Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro
410 415

<210> 2
<211> 461
<212> PRT
<213> Homo sapiens

<400> 2
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-40 -35 -30

Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg
-25 -20 -15

Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
-10 -5 -1 1 5

Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys
10 15 20

Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu
25 30 35

Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro
40 45 50

Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile
55 60 65 70

Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly
75 80 85

Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn
90 95 100

Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys
105 110 115

Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His
120 125 130

Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys
135 140 145 150

Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val
155 160 165

Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro
170 175 180

Trp Gln Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala
185 190 195

Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp
200 205 210

Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg

00997623.112901

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215 220 225 230

Trp Glu Lys Trp Glu₂₃₅ Leu Asp Leu Asp Ile₂₄₀ Lys Glu Val Phe Val₂₄₅ His

Pro Asn Tyr Ser₂₅₀ Lys Ser Thr Thr Asp₂₅₅ Asn Asp Ile Ala Leu₂₆₀ Leu His

Leu Ala Gln₂₆₅ Pro Ala Thr Leu Ser₂₇₀ Gln Thr Ile Val Pro₂₇₅ Ile Cys Leu

Pro Asp₂₈₀ Ser Gly Leu Ala Glu₂₈₅ Arg Glu Leu Asn Gln₂₉₀ Ala Gly Gln Glu

Thr₂₉₅ Leu Val Thr Gly Trp₃₀₀ Gly Tyr His Ser Ser₃₀₅ Arg Glu Lys Glu Ala₃₁₀

Lys Arg Asn Arg Thr₃₁₅ Phe Val Leu Asn Phe₃₂₀ Ile Lys Ile Pro Val₃₂₅ Val

Pro His Asn Glu₃₃₀ Cys Ser Glu Val Met₃₃₅ Ser Asn Met Val₃₄₀ Ser Glu Asn

Met Leu Cys₃₄₅ Ala Gly Ile Leu Gly₃₅₀ Asp Arg Gln Asp Ala₃₅₅ Cys Glu Gly

Asp Ser₃₆₀ Gly Gly Pro Met Val₃₆₅ Ala Ser Phe His Gly₃₇₀ Thr Trp Phe Leu

Val₃₇₅ Gly Leu Val Ser Trp₃₈₀ Gly Glu Gly Cys Gly₃₈₅ Leu Leu His Asn Tyr₃₉₀

Gly Val Tyr Thr Lys₃₉₅ Val Ser Arg Tyr Leu₄₀₀ Asp Trp Ile His Gly₄₀₅ His

Ile Arg Asp Lys₄₁₀ Glu Ala Pro Gln Lys₄₁₅ Ser Trp Ala Pro

<210> 3
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1257)

<400> 3

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Ala Asn Ser Phe Leu ₅ Glu Glu Leu Arg His ₁₀ Ser Ser Leu Glu Arg ₁₅ Glu	
tgc ata gag gag atc tgt gac ttc gag gag gcc aag gaa att ttc caa	96
Cys Ile Glu ₂₀ Glu Ile Cys Asp Phe ₂₅ Glu Glu Ala Lys Glu ₃₀ Ile Phe Gln	
aat gtg gat gac aca ctg gcc ttc tgg tcc aag cac gtc gac ggt gac	144
Asn Val ₃₅ Asp Thr Leu Ala ₄₀ Phe Trp Ser Lys His ₄₅ Val Asp Gly Asp	
cag tgc ttg gtc ttg ccc ttg gag cac ccg tgc gcc agc ctg tgc tgc	192
Gln ₅₀ Cys Leu Val Leu Pro ₅₅ Glu His Pro Cys ₆₀ Ala Ser Leu Cys Cys	
ggg cac ggc acg tgc atc gac ggc atc ggc agc ttc agc tgc gac tgc	240

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Gly His Gly Thr Cys Ile Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys
 65 70 75 80
 cgc agc ggc tgg gag ggc cgc ttc tgc cag cgc gag gtg agc ttc ctc 288
 Arg Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg Glu Val Ser Phe Leu
 85 90 95
 aat tgc tcg ctg gac aac ggc ggc tgc acg cat tac tgc cta gag gag 336
 Asn Cys Ser Leu Asp Asn Gly Gly Cys Thr His Tyr Cys Leu Glu Glu
 100 105 110
 gtg ggc tgg cgg cgc tgt agc tgt gcg cct ggc tac aag ctg ggg gac 384
 Val Gly Trp Arg Arg Cys Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp
 115 120 125
 gac ctc ctg cag tgt cac ccc gca gtg aag ttc cct tgt ggg agg ccc 432
 Asp Leu Leu Gln Cys His Pro Ala Val Lys Phe Pro Cys Gly Arg Pro
 130 135 140
 tgg aag cgg atg gag aag aag cgc agt cac ctg aaa cga gac aca gaa 480
 Trp Lys Arg Met Glu Lys Lys Arg Ser His Lys Lys Arg Asp Thr Glu
 145 150 155 160
 gac caa gaa gac caa gta gat ccg cgg ctc att gat ggg aag atg acc 528
 Asp Gln Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys Met Thr
 165 170 175
 agg cgg gga gac agc ccc tgg cag gtg gtc ctg ctg gac tca aag aag 576
 Arg Arg Gly Asp Ser Pro Trp Gln Val Val Leu Leu Asp Ser Lys Lys
 180 185 190
 aag ctg gcc tgc ggg gca gtg ctc atc cac ccc tcc tgg gtg ctg aca 624
 Lys Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr
 195 200 205
 gcg gcc cac tgc atg gat gag tcc aag aag ctc ctt gtc agg ctt gga 672
 Ala Ala His Cys Met Asp Glu Ser Lys Lys Leu Leu Val Arg Leu Gly
 210 215 220
 gag tat gac ctg cgg cgc tgg gag aag tgg gag ctg gac ctg gac atc 720
 Glu Tyr Asp Leu Arg Arg Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile
 225 230 235 240
 aag gag gtc ttc gtc cac ccc aac tac agc aag agc acc acc gac aat 768
 Lys Glu Val Phe Val His Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn
 245 250 255
 gac atc gca ctg ctg cac ctg gcc cag ccc gcc acc ctc tcg cag acc 816
 Asp Ile Ala Leu Leu His Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr
 260 265 270
 ata gtg ccc atc tgc ctc ccg gac agc ggc ctt gca gag cgc gag ctc 864
 Ile Val Pro Ile Cys Leu Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu
 275 280 285
 aat cag gcc ggc cag gag acc ctc gtg acg ggc tgg ggc tac cac agc 912
 Asn Gln Ala Gly Gln Glu Thr Leu Val Thr Gly Trp Gly Tyr His Ser
 290 295 300
 agc cga gag aag gag gcc aag aga aac cgc acc ttc gtc ctc aac ttc 960
 Ser Arg Glu Lys Glu Ala Lys Arg Asn Arg Thr Phe Val Leu Asn Phe
 305 310 315 320
 atc aag att ccc gtg gtc ccg cac aat gag tgc agc gag gtc atg agc 1008
 Ile Lys Ile Pro Val Val Pro His Asn Glu Cys Ser Glu Val Met Ser
 325 330 335

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aac atg gtg tct gag aac atg ctg tgt gcg ggc atc ctc ggg gac cgg 1056
 Asn Met Val Ser Glu Asn Met Leu Cys Ala Gly Ile Leu Gly Asp Arg
 340 345 350
 cag gat gcc tgc gag ggc gac agt ggg ggg ccc atg gtc gcc tcc ttc 1104
 Gln Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Met Val Ala Ser Phe
 355 360 365
 cac ggc acc tgg ttc ctg gtg ggc ctg gtg agc tgg ggt gag ggc tgt 1152
 His Gly Thr Trp Phe Leu Val Gly Leu Val Ser Trp Gly Glu Gly Cys
 370 375 380
 ggg ctc ctt cac aac tac ggc gtt tac acc aaa gtc agc cgc tac ctc 1200
 Gly Leu Leu His Asn Tyr Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu
 385 390 395 400
 gac tgg atc cat ggg cac atc aga gac aag gaa gcc ccc cag aag agc 1248
 Asp Trp Ile His Gly His Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser
 405 410 415
 tgg gca cct 1257
 Trp Ala Pro

<210> 4
 <211> 419
 <212> PRT
 <213> Homo sapiens

<400> 4
 Ala Asn Ser Phe Leu Glu Glu Leu Arg His Ser Ser Leu Glu Arg Glu
 1 5 10 15
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 20 25 30
 Asn Val Asp Asp Thr Leu Ala Phe Trp Ser Lys His Val Asp Gly Asp
 35 40 45
 Gln Cys Leu Val Leu Pro Leu Glu His Pro Cys Ala Ser Leu Cys Cys
 50 55 60
 Gly His Gly Thr Cys Ile Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys
 65 70 75 80
 Arg Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg Glu Val Ser Phe Leu
 85 90 95
 Asn Cys Ser Leu Asp Asn Gly Gly Cys Thr His Tyr Cys Leu Glu Glu
 100 105 110
 Val Gly Trp Arg Arg Cys Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp
 115 120 125
 Asp Leu Leu Gln Cys His Pro Ala Val Lys Phe Pro Cys Gly Arg Pro
 130 135 140
 Trp Lys Arg Met Glu Lys Lys Arg Ser His Leu Lys Arg Asp Thr Glu
 145 150 155 160
 Asp Gln Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys Met Thr
 165 170 175
 Arg Arg Gly Asp Ser Pro Trp Gln Val Val Leu Leu Asp Ser Lys Lys
 180 185 190
 Lys Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr

195

Ala Ala His Cys Met Asp Glu Ser Lys Lys Leu Leu Val Arg Leu Gly
210 215 220
Glu Tyr Asp Leu Arg Arg Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile
225 230 235 240
Lys Glu Val Phe Val His Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn
245 250 255
Asp Ile Ala Leu Leu His Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr
260 265 270
Ile Val Pro Ile Cys Leu Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu
275 280 285
Asn Gln Ala Gly Gln Glu Thr Leu Val Thr Gly Trp Gly Tyr His Ser
290 295 300
Ser Arg Glu Lys Glu Ala Lys Arg Asn Arg Thr Phe Val Leu Asn Phe
305 310 315 320
Ile Lys Ile Pro Val Val Pro His Asn Glu Cys Ser Glu Val Met Ser
325 330 335
Asn Met Val Ser Glu Asn Met Leu Cys Ala Gly Ile Leu Gly Asp Arg
340 345 350
Gln Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Met Val Ala Ser Phe
355 360 365
His Gly Thr Trp Phe Leu Val Gly Leu Val Ser Trp Gly Glu Gly Cys
370 375 380
Gly Leu Leu His Asn Tyr Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu
385 390 395 400
Asp Trp Ile His Gly His Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser
405 410 415
Trp Ala Pro

<210> 5
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 5
caagtagatc cgcggctcat taacgggaag atgaccaggc gggg

44

<210> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6

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<210> 7
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
ctgacagcgg ccactgcat gaacgagtcc aagaagctcc ttgtc 45

<210> 8
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
gacaaggagc ttcttgact cgttcacgca gtgggcccgt gtcag 45

<210> 9
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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ctgacagcgg ccactgcat ggccgagtcc aagaagctcc ttgtc 45

<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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gacaaggagc ttcttgact cggccatgca gtgggcccgt gtcag 45

<210> 11
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
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cttcgtccac cccaactaca gcaacagcac caccgacaat gacatc 46

<210> 12
<211> 46
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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46

<210> 13

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

cgccacccc aactacagca agaacaccac cgacaatgac atcgc

45

<210> 14

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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gcgatgtcat tgctcgggtgtt gttcttgctg tagttgggggt ggacg

45

<210> 15

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 16

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 17

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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cagcgaggtc atgagcaaca acgtgtctga gaacatgc

38

<210> 18

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<211> 38
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Primer
 <400> 18
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<210> 19
 <211> 39
 <212> DNA
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 <400> 19
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<210> 20
 <211> 39
 <212> DNA
 <213> Artificial Sequence
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 <400> 20
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<210> 21
 <211> 50
 <212> DNA
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 <223> Description of Artificial Sequence: Primer
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<210> 22
 <211> 50
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<210> 23
 <211> 50
 <212> DNA
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<400> 23
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<210> 24
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
ccccgcaggc cagcttcttg gttgagttca gcaggaccac ctgcc 45

<210> 25
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
ggcaggtggt cctgctggac aacaagacca agctggcctg cggggcagt 49

<210> 26
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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gcactgcccc gcaggccagc ttggtcttgt tgtccagcag gaccacctgc c 51

<210> 27
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
gtcctgctgg actcaaaca gaccctggcc tgcggggcag tg 42

<210> 28
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
cactgccccg caggccaggg tcttgtttga gtccagcagg ac 42

<210> 29
<211> 48
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

gcatggatga gtccaacaag acccttgatca ggcttggaga gtatgacc 48

<210> 30

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30

ggtcatactc tccaagcctg acaagggtct tgttggactc atccatgc 48

<210> 31

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31

ccaactacag caagagcaac accaccaatg acatcgact gctgcacctg 50

<210> 32

<211> 52

<212> DNA

<213> Artificial Sequence

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<210> 33

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

ggctggggct accacagcaa ccgaaccaag gaggccaaga gaaaccgc 48

<210> 34

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 34

gcggtttctc ttggcctcct tggttcggtt gctgtggtag ccccagcc 48

<210> 35
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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Primer

<400> 35
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<210> 36
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 36
 cgaaggtgcg gtttctcttg gcggtcttgt ttcggctgct gtggtagcc 49

<210> 37
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 37
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<210> 38
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 38
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<210> 39
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 39
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<210> 40
 <211> 52
 <212> DNA
 <213> Artificial Sequence

0219us410-sequence.txt

<220>

<223> Description of Artificial Sequence: Primer

<400> 40

ggtgtaaacg ccgtagttgg taagggtccc acagccctca cccagctca cc

52

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